



2024 Influenza A Virus HPAI H5N1 Outbreak Weekly Report June 12, 2024

Introduction

In March 2024, several cases of highly pathogenic avian influenza A (HPAI) H5N1 virus were confirmed in dairy cattle in Texas, with cases spreading to at least eight other states (<https://www.biorxiv.org/content/10.1101/2024.05.01.591751v1>). In addition, a human case of influenza from the same clade and genotype was also diagnosed in a dairy worker from Texas around the same time. As part of an effort to track this outbreak, the United States Department of Agriculture (USDA) Agricultural Research Service (ARS) and the USDA National Veterinary Services Laboratories (NVSL) have been working to collect and sequence samples from additional cattle as well as avian species and other animals that also appeared to be infected with HPAI that might be related to the virus from the Texas dairy cattle. The genomic sequences of each virus isolate (consisting of the eight genomic segments sequenced for each individual isolate) are assembled from the sequenced short read data, and after undergoing quality control, are submitted to the GenBank sequence repository where they become publicly available. To enhance the ability of the USDA to rapidly submit sequences to GenBank, personnel from the Bacterial and Viral Bioinformatics Resource Center (BV-BRC) have been collaborating with USDA scientists to assist them with the submission of assembled HPAI genomic sequences to GenBank.

The BV-BRC provides a database of complete and partially sequenced microbial genomes from both viral and bacterial pathogens. This data is derived from the GenBank repository and includes metadata obtained from the GenBank record as well as associated NCBI BioProject, BioSample, and SRA repository records. All this metadata provides users with the ability to search for specific datasets from the BV-BRC web site using the filtering and sorting features built into BV-BRC web-retrieval tools. To provide rapid access to sequences and other data and information from the 2024 HPAI outbreak, the BV-BRC provides an outbreak-specific web page with links to this information: (https://www.bv-brc.org/outbreaks/H5N1/#view_tab=overview).

This report provides statistics on the public availability of HPAI H5N1 genomic sequences historically, and especially from isolates collected since 2024 in North America.

Updates

- On May 30, the US reported a second case of human H5N associated with the dairy cow outbreak in Michigan (<https://www.cdc.gov/media/releases/2024/p0530-h5-human-case-michigan.html>), bringing the total number of dairy cattle-associated 2024 human cases to three. Sequences of the genomes from these human isolates can be found in the [BV-BRC database](#). Note that only two segments (HA-4 and NA-6) from the second human case in Michigan are currently available.

Statistics (As of June 10, 2024)

The numbers provided below are obtained from the BV-BRC database. These numbers should be equivalent to those available from GenBank with the exception that newly submitted sequences may take a few days to be available from the BV-BRC database. For the 2024 outbreak, where we have isolate-specific information, we report the number of isolates along with the number of sequenced genomic segments (generally 8 per isolate). These numbers include sequences generated by the USDA and submitted to GenBank by both the USDA and BV-BRC, USDA sequences assembled by the BV-BRC from SRA data not yet submitted to GenBank, and sequences submitted to GenBank from all other sources.

Influenza A sequence counts from the BV-BRC database

| Outbreak Report | All Influenza A Sequences | All H5N1 Sequences | 2024 H5N1 Sequences |
|-----------------|---------------------------|------------------------|--------------------------------------|
| May 22 | 1,061,803 | 53,046 | 2,395 (298 isolates) |
| May 29 | 1,065,779 | 54,648 | 2,579 (320 isolates) |
| June 12* | 1,082,514 | 57,317 | 5,148 (643 isolates) |

*The BV-BRC genomic database links provided for the most recent totals will provide numbers as of the time the link is followed. Therefore, these numbers will increase over time.

Influenza A sequences from SRA and not yet submitted to GenBank

On June 7, 2024 the BV-BRC began a search for influenza A sequence data that had been submitted as raw data into the NCBI SRA (sequence read archive) database, but had not yet been assembled and submitted to GenBank. The search was for records deposited in 2024 (though not necessarily collected in 2024). The results of that search were as follows:

Influenza A Virus Records in SRA and GenBank Released in 2024

- 90,630 Total GenBank records for Influenza A virus from 2024
- 3,229 Total SRA records for Influenza A virus from 2024
- 901 SRA records are linked to GenBank records
- 2,328 SRA records are not linked to GenBank records

The BV-BRC downloaded the 2,328 SRA records and ran them through our influenza A assembly pipeline using the IRMA assembler. These genomic sequences have been uploaded into the BV-BRC database and can be accessed through the [BV-BRC Genome tab](#). The remaining unassembled SRA records produced errors during the assembly process. These will have to be resolved before the assembled sequences can be added to our analysis and the BV-BRC database.

The SRA samples were collected between 2013 and 2024. Of the 290 H5N1 samples, 289 were collected in 2024. Of these, 2 were deposited by Iowa State, and 287 were deposited by the USDA. The results of the SRA assembly process was as follows:

SRA samples assembled by the BV-BRC

| Subtype | Samples | Segments Assembled |
|--------------|--------------|--------------------|
| H1N1 | 657 | 5141 |
| H1N7 | 9 | 72 |
| H3N2 | 462 | 3676 |
| H5N1 | 290 | 2320 |
| H6N7 | 9 | 72 |
| Unknown | 56 | 328 |
| Total | 1,483 | 11,609 |

SRA samples by Subtype and Year

| Subtype | Year | Segments |
|----------------|--------|----------|
| Unknown | Total: | 328 |
| | 2013 | 3 |
| | 2022 | 44 |
| | 2023 | 243 |
| | 2024 | 35 |
| | - | 3 |
| H1N1 | Total: | 5141 |
| | 2013 | 8 |
| | 2019 | 144 |
| | 2022 | 95 |
| | 2023 | 3126 |
| | 2024 | 1696 |
| | - | 72 |
| H1N7 | Total: | 72 |
| | 2023 | 72 |
| H3N2 | Total: | 3676 |
| | 2013 | 999 |
| | 2022 | 294 |
| | 2023 | 1225 |
| | 2024 | 1158 |
| H5N1 | Total: | 2320 |
| | 2023 | 8 |
| | 2024 | 2312 |
| H6N7 | Total: | 72 |
| | 2023 | 72 |
| Total | | 11609 |

These tables summarize all sequences available as of June 10, 2024 and includes both GenBank and SRA-derived isolates.

H5N1 US virus isolates collected and sequenced in 2024, by host and US states:

| Host | # Samples |
|------------------------|------------------|
| American Crow | 3 |
| American white pelican | 1 |
| American Wigeon | 1 |
| Bald Eagle | 3 |
| Blackbird | 2 |
| CAGO | 1 |
| Canada Goose | 3 |
| Cat | 2 |
| Chicken | 59 |
| Common Grackle | 1 |
| Common Raven | 2 |
| Cow | 378 |
| Crow | 5 |
| Domestic Cat | 32 |
| Duck | 2 |
| Ganada Goose | 1 |
| Goat | 30 |
| Goose | 9 |
| Grackle | 3 |
| Great Horned Owl | 1 |
| Great horned owl/ | 1 |
| Harris Hawk | 1 |
| Harris-Hawk | 1 |
| Hawk | 5 |
| Hooded Merganser | 1 |
| Human | 2 |
| Mallard | 2 |
| Mountain Lion | 4 |
| Mute Swan | 2 |
| Pefa | 1 |
| Peregrine Falcon | 1 |
| Pigeon | 2 |
| Raccoon | 4 |
| Red Fox | 5 |
| Red Tailed Hawk | 3 |
| Redhead duck | 3 |
| Ruddy Turnstone | 1 |
| Sanderling | 8 |
| Skunk | 18 |
| Snow Goose | 6 |
| Turkey | 30 |
| Turkey Vulture | 2 |
| Western Gull | 2 |
| Western Sandpiper | 1 |
| Wood duck | 1 |

| State | # Samples |
|----------------|------------------|
| California | 8 |
| Colorado | 1 |
| Idaho | 6 |
| Illinois | 2 |
| Indiana | 5 |
| Iowa | 1 |
| Kansas | 15 |
| Maryland | 2 |
| Michigan | 25 |
| Minnesota | 21 |
| Missouri | 7 |
| Montana | 4 |
| New Mexico | 32 |
| North Carolina | 12 |
| Ohio | 30 |
| Oklahoma | 1 |
| Oregon | 3 |
| South Carolina | 3 |
| South Dakota | 21 |
| Texas | 139 |
| USA | 294 |
| Utah | 2 |
| Virginia | 6 |
| Washington | 7 |

Phylogenetic Analysis

- The latest phylogenetic trees for all eight segments can be accessed using the URL below, which includes all human isolates with available sequence data.
https://www.bv-brc.org/outbreaks/H5N1/#view_tab=phylogenetics

News

| Title | Date | Source |
|---|---------|----------|
| H9N2 avian flu infects children in India, China | June 11 | CIDRAP |
| USDA reports more H5N1 detections in mice and cats | June 11 | CIDRAP |
| Bird flu: Australia records first human case of H5N1 | June 10 | The BMJ |
| Study shows 'not surprising' fatal spread of avian flu in ferrets | June 10 | CIDRAP |
| Huge amounts of bird-flu virus found in raw milk of infected cows | June 5 | Nature |
| Elephant seal outbreak marks first transnational spread of highly pathogenic avian influenza in mammals | June 5 | PHYS.org |
| Information for Farm Workers Exposed to H5N1 Bird Flu in Dairy Cows | June 5 | CDC |
| Avian Influenza A (H5N2) - Mexico | June 4 | WHO |
| Avian flu strikes more Minnesota poultry farms | June 4 | CIDRAP |
| H5 influenza wastewater dashboard launches | June 3 | CIDRAP |
| Unpasteurized (Raw) Milk and Highly Pathogenic Avian Influenza | June 3 | CDC |
| Bird Flu Virus Infections in Humans Avian Influenza | May 30 | CDC |
| Outbreak of Highly Pathogenic Avian Influenza A(H5N1) Viruses in U.S. Dairy Cattle and Detection of Two Human | May 30 | CDC |
| US nears deal to fund Moderna's bird flu vaccine trial, FT reports | May 30 | Reuters |
| To probe outbreak, BSL-3 labs plan to infect cows with flu virus | May 10 | Science |
| Feds announces assistance for US farmers affected by H5N1 avian flu | May 10 | CIDRAP |
| Updates on Highly Pathogenic Avian Influenza (HPAI) | May 10 | FDA |

Publications

| Title | Date | Source |
|--|---------|--|
| Sialic Acid Receptor Specificity in Mammary Gland of Dairy Cattle Infected with Highly Pathogenic Avian Influenza A(H5N1) Virus. | June 11 | Emerging Infectious Disease |
| Influenza virus uses mGluR2 as an endocytic receptor to enter cells | June 7 | Nature |
| N-glycosylation on hemagglutinin head reveals inter-branch antigenic variability of avian influenza virus H5-subtypes | June 5 | International Journal of Biological Macromolecules |
| Avian influenza viruses in New Zealand wild birds, with an emphasis on subtypes H5 and H7: Their distinctive epidemiology and genomic properties | June 3 | PLOS One |

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|---|---------------|----------------------------------|
| Avian Influenza A(H5N1) Virus among Dairy Cattle, Texas, USA | Early Release | CDC |
| Deep mutational scanning of H5 hemagglutinin to inform influenza virus surveillance | Pre-print | bioRxiv |
| Rapid mortality in captive bush dogs (Speothos venaticus) caused by influenza A of avian origin (H5N1) at a wildlife collection in the United Kingdom | May 27 | Emerging microbes and infections |